



SEQUENCE LISTING

<110> LAU, Lester

<120> EXTRACELLULAR MATRIX SIGNALLING MOLECULES

<130> 28758/36072

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<150> 09/142,569

<151> 1999-04-02

<150> 60/013,958

<151> 1996-03-15

<160> 34

<170> PatentIn Ver. 2.0

<210> 1

<211> 1480

<212> DNA

<213> Mus musculus

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<221> CDS

<222> (180)..(1316)

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<223> Mouse cyr61 cDNA coding sequence

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ctcgccggct tgttggttct gtgtcgccgc gctcgccccg gttcctcctg cgcgccaca 179
atg agc tcc agc acc ttc agg acg ctc gct gtc gcc gtc acc ctt ctc 227
Met Ser Ser Ser Thr Phe Arg Thr Leu Ala Val Ala Val Thr Leu Leu
1 5 10 15
cac ttg acc aga ctg gcg ctc tcc acc tgc ccc gcc gcc tgc cac tgc 275
His Leu Thr Arg Leu Ala Leu Ser Thr Cys Pro Ala Ala Cys His Cys
20 25 30
cct ctg gag gca ccc aag tgc gcc ccg gga gtc ggg ttg gtc cgg gac 323
Pro Leu Glu Ala Pro Lys Cys Ala Pro Gly Val Gly Leu Val Arg Asp
35 40 45
ggc tgc ggc tgc tgt aag gtc tgc gct aaa caa ctc aac gag gac tgc 371
Gly Cys Gly Cys Cys Lys Val Cys Ala Lys Gln Leu Asn Glu Asp Cys
50 55 60
agc aaa act cag ccc tgc gac cac acc aag ggg ttg gaa tgc aat ttc 419
Ser Lys Thr Gln Pro Cys Asp His Thr Lys Gly Leu Glu Cys Asn Phe
65 70 75 80
ggc gcc agc tcc acc gct ctg aaa ggg atc tgc aga gct cag tca gaa 467
Gly Ala Ser Ser Thr Ala Leu Lys Gly Ile Cys Arg Ala Gln Ser Glu
85 90 95
ggc aga ccc tgt gaa tat aac tcc aga atc tac caa aac ggg gaa agc 515

Gly	Arg	Pro	Cys 100	Glu	Tyr	Asn	Ser	Arg 105	Ile	Tyr	Gln	Asn	Gly 110	Glu	Ser		
ttc	cag	ccc	aac	tgt	aaa	cac	cag	tgc	aca	tgt	att	gat	ggc	gcc	gtg	563	
Phe	Gln	Pro	Asn	Cys	Lys	His	Gln 120	Cys	Thr	Cys	Ile	Asp 125	Gly	Ala	Val		
ggc	tgc	att	cct	ctg	tgt	ccc	caa	gaa	ctg	tct	ctc	ccc	aat	ctg	ggc	611	
Gly	Cys 130	Ile	Pro	Leu	Cys	Pro 135	Gln	Glu	Leu	Ser	Leu 140	Pro	Asn	Leu	Gly		
tgt	ccc	aac	ccc	cgg	ctg	gtg	aaa	gtc	agc	ggg	cag	tgc	tgt	gaa	gag	659	
Cys 145	Pro	Asn	Pro	Arg	Leu 150	Val	Lys	Val	Ser	Gly 155	Gln	Cys	Cys	Glu	Glu 160		
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Trp	Val	Cys	Asp	Glu 165	Asp	Ser	Ile	Lys	Asp 170	Ser	Leu	Asp	Asp	Gln 175	Asp		
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gag	tta	atc	gca	att	gga	aaa	ggc	agc	tca	ctg	aag	agg	ctt	cct	gtc	803	
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Phe	Gly 210	Thr	Glu	Pro	Arg	Val 215	Leu	Phe	Asn	Pro	Leu 220	His	Ala	His	Gly		
cag	aaa	tgc	atc	gtt	cag	acc	acg	tct	tgg	tcc	cag	tgc	tcc	aag	agc	899	
Gln 225	Lys	Cys	Ile	Val	Gln 230	Thr	Thr	Ser	Trp	Ser 235	Gln	Cys	Ser	Lys	Ser 240		
tgc	gga	act	ggc	atc	tcc	aca	cga	gtt	acc	aat	gac	aac	cca	gag	tgc	947	
Cys	Gly	Thr	Gly	Ile 245	Ser	Thr	Arg	Val	Thr 250	Asn	Asp	Asn	Pro	Glu 255	Cys		
cgc	ctg	gtg	aaa	gag	acc	cgg	atc	tgt	gaa	gtg	cgt	cct	tgt	gga	caa	995	
Arg	Leu	Val	Lys 260	Glu	Thr	Arg	Ile	Cys 265	Glu	Val	Arg	Pro	Cys 270	Gly	Gln		
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Pro	Val	Tyr 275	Ser	Ser	Leu	Lys	Lys 280	Gly	Lys	Lys	Cys	Ser 285	Lys	Thr	Lys		
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Lys	Ser 290	Pro	Glu	Pro	Val	Arg 295	Phe	Thr	Tyr	Ala	Gly 300	Cys	Ser	Ser	Val		
aag	aaa	tac	cgg	ccc	aaa	tac	tgc	ggc	tcc	tgc	gta	gat	ggc	cgg	tgc	1139	
Lys 305	Lys	Tyr	Arg	Pro	Lys 310	Tyr	Cys	Gly	Ser	Cys 315	Val	Asp	Gly	Arg	Cys 320		
tgc	aca	cct	ctg	cag	acc	aga	act	gtg	aag	atg	cgg	ttc	cga	tgc	gaa	1187	
Cys	Thr	Pro	Leu	Gln 325	Thr	Arg	Thr	Val	Lys 330	Met	Arg	Phe	Arg	Cys 335	Glu		
gat	gga	gag	atg	ttt	tcc	aag	aat	gtc	atg	atg	atc	cag	tcc	tgc	aaa	1235	
Asp	Gly	Glu	Met 340	Phe	Ser	Lys	Asn	Val 345	Met	Met	Ile	Gln	Ser	Cys	Lys		
tgt	aac	tac	aac	tgc	ccg	cat	ccc	aac	gag	gca	tcg	ttc	cga	ctg	tac	1283	
Cys	Asn	Tyr	Asn	Cys	Pro	His	Pro	Asn	Glu	Ala	Ser	Phe	Arg	Leu	Tyr		

355

360

365

agc cta ttc aat gac atc cac aag ttc agg gac taagtgcctc cagggttcct 1336
 Ser Leu Phe Asn Asp Ile His Lys Phe Arg Asp
 370 375

agtgtgggct ggacagagga gaagcgcaag catcatggag acgtgggtgg gcggaggatg 1396

aatggtgcct tgctcattct tgagtagcat tagggatattt caaaactgcc aaggggctga 1456

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<211> 379

<212> PRT

<213> Mus musculus

<400> 2

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Pro Leu Glu Ala Pro Lys Cys Ala Pro Gly Val Gly Leu Val Arg Asp
 35 40 45

Gly Cys Gly Cys Cys Lys Val Cys Ala Lys Gln Leu Asn Glu Asp Cys
 50 55 60

Ser Lys Thr Gln Pro Cys Asp His Thr Lys Gly Leu Glu Cys Asn Phe
 65 70 75 80

Gly Ala Ser Ser Thr Ala Leu Lys Gly Ile Cys Arg Ala Gln Ser Glu
 85 90 95

Gly Arg Pro Cys Glu Tyr Asn Ser Arg Ile Tyr Gln Asn Gly Glu Ser
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Phe Gln Pro Asn Cys Lys His Gln Cys Thr Cys Ile Asp Gly Ala Val
 115 120 125

Gly Cys Ile Pro Leu Cys Pro Gln Glu Leu Ser Leu Pro Asn Leu Gly
 130 135 140

Cys Pro Asn Pro Arg Leu Val Lys Val Ser Gly Gln Cys Cys Glu Glu
 145 150 155 160

Trp Val Cys Asp Glu Asp Ser Ile Lys Asp Ser Leu Asp Asp Gln Asp
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Asp Leu Leu Gly Leu Asp Ala Ser Glu Val Glu Leu Thr Arg Asn Asn
 180 185 190

Glu Leu Ile Ala Ile Gly Lys Gly Ser Ser Leu Lys Arg Leu Pro Val
 195 200 205

Phe Gly Thr Glu Pro Arg Val Leu Phe Asn Pro Leu His Ala His Gly
 210 215 220

Gln Lys Cys Ile Val Gln Thr Thr Ser Trp Ser Gln Cys Ser Lys Ser
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Cys Gly Thr Gly Ile Ser Thr Arg Val Thr Asn Asp Asn Pro Glu Cys

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agt Ser	ttc Phe	cag Gln	ccc Pro 115	aac Asn	tgt Cys	caa Gln	cat His	cag Gln 120	tgc Cys	aca Thr	tgt Cys	att Ile	gat Asp 125	ggc Gly	gcc Ala	504
gtg Val	ggc Gly	tgc Cys 130	att Ile	cct Pro	ctg Leu	tgt Cys	ccc Pro 135	caa Gln	gaa Glu	cta Leu	tct Ser	ctc Leu 140	ccc Pro	aac Asn	ttg Leu	552
ggc Gly 145	tgt Cys	ccc Pro	aac Asn	cct Pro	cgg Arg	ctg Leu 150	gtc Val	aaa Lys	gtt Val	acc Thr	ggg Gly 155	cag Gln	tgc Cys	tgc Cys	gag Glu	600
gag Glu 160	tgg Trp	gtc Val	tgt Cys	gac Asp	gag Glu 165	gat Asp	agt Ser	atc Ile	aag Lys	gac Asp 170	ccc Pro	atg Met	gag Glu	gac Asp	cag Gln 175	648
gac Asp	ggc Gly	ctc Leu	ctt Leu	ggc Gly 180	aag Lys	gag Glu	ctg Leu	gga Gly	ttc Phe 185	gat Asp	gcc Ala	tcc Ser	gag Glu	gtg Val 190	gag Glu	696
ttg Leu	acg Thr	aga Arg	aac Asn 195	aat Asn	gaa Glu	ttg Leu	att Ile	gca Ala 200	gtt Val	gga Gly	aaa Lys	ggc Gly	aga Arg 205	tca Ser	ctg Leu	744
aag Lys	cgg Arg	ctc Leu 210	cct Pro	gtt Val	ttt Phe	gga Gly	atg Met 215	gag Glu	cct Pro	cgc Arg	atc Ile	cta Leu 220	tac Tyr	aac Asn	cct Pro	792
tta Leu 225	caa Gln	ggc Gly	cag Gln	aaa Lys	tgt Cys	att Ile 230	gtt Val	caa Gln	aca Thr	act Thr	tca Ser 235	tgg Trp	tcc Ser	cag Gln	tgc Cys	840
tca Ser 240	aag Lys	acc Thr	tgt Cys	gga Gly 245	act Thr	ggt Gly	atc Ile	tcc Ser	aca Thr	cga Arg 250	gtt Val	acc Thr	aat Asn	gac Asp 255	aac Asn	888
cct Pro	gag Glu	tgc Cys	cgc Arg	ctt Leu 260	gtg Val	aaa Lys	gaa Glu	acc Thr	cgg Arg 265	att Ile	tgt Cys	gag Glu	gtg Val	cgg Arg 270	cct Pro	936
tgt Cys	gga Gly	cag Gln	cca Pro 275	gtg Val	tac Tyr	agc Ser	agc Ser	ctg Leu 280	aaa Lys	aag Lys	ggc Gly	aag Lys	aaa Lys 285	tgc Cys	agc Ser	984
aag Lys	acc Thr	aag Lys 290	aaa Lys	tcc Ser	ccc Pro	gaa Glu	cca Pro 295	gtc Val	agg Arg	ttt Phe	act Thr	tac Tyr 300	gct Ala	gga Gly	tgt Cys	1032
ttg Leu	agt Ser 305	gtg Val	aag Lys	aaa Lys	tac Tyr	cgg Arg 310	ccc Pro	aag Lys	tac Tyr	tgc Cys	ggt Gly 315	tcc Ser	tgc Cys	gtg Val	gac Asp	1080
ggc Gly 320	cga Arg	tgc Cys	tgc Cys	acg Thr	ccc Pro 325	cag Gln	ctg Leu	acc Thr	agg Arg	act Thr 330	gtg Val	aag Lys	atg Met	cgg Arg	ttc Phe 335	1128
cgc Arg	tgc Cys	gaa Glu	gat Asp	ggg Gly	gag Glu	aca Thr	ttt Phe	tcc Ser	aag Lys	aac Asn	gtc Val	atg Met	atg Met	atc Ile	cag Gln	1176

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Ser Cys Lys Cys Asn Tyr Asn Cys Pro His Ala Asn Glu Ala Ala Phe			
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ccc ttc tac agg ctg ttc aat gac att cac aaa ttt agg gac			1266
Pro Phe Tyr Arg Leu Phe Asn Asp Ile His Lys Phe Arg Asp			
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 <213> Homo sapiens

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 35 40 45
 Gly Cys Gly Cys Cys Lys Val Cys Ala Lys Gln Leu Asn Glu Asp Cys
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 Ser Lys Thr Gln Pro Cys Asp His Thr Lys Gly Leu Glu Cys Asn Phe
 65 70 75 80
 Gly Ala Ser Ser Thr Ala Leu Lys Gly Ile Cys Arg Ala Gln Ser Glu
 85 90 95
 Gly Arg Pro Cys Glu Tyr Asn Ser Arg Ile Tyr Gln Asn Gly Glu Ser
 100 105 110
 Phe Gln Pro Asn Cys Gln His Gln Cys Thr Cys Ile Asp Gly Ala Val
 115 120 125
 Gly Cys Ile Pro Leu Cys Pro Gln Glu Leu Ser Leu Pro Asn Leu Gly
 130 135 140
 Cys Pro Asn Pro Arg Leu Val Lys Val Thr Gly Gln Cys Cys Glu Glu
 145 150 155 160
 Trp Val Cys Asp Glu Asp Ser Ile Lys Asp Pro Met Glu Asp Gln Asp
 165 170 175
 Gly Leu Leu Gly Lys Glu Leu Gly Phe Asp Ala Ser Glu Val Glu Leu
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 Thr Arg Asn Asn Glu Leu Ile Ala Val Gly Lys Gly Arg Ser Leu Lys
 195 200 205
 Arg Leu Pro Val Phe Gly Met Glu Pro Arg Ile Leu Tyr Asn Pro Leu
 210 215 220

Gln Gly Gln Lys Cys Ile Val Gln Thr Thr Ser Trp Ser Gln Cys Ser
 225 230 235 240
 Lys Thr Cys Gly Thr Gly Ile Ser Thr Arg Val Thr Asn Asp Asn Pro
 245 250 255
 Glu Cys Arg Leu Val Lys Glu Thr Arg Ile Cys Glu Val Arg Pro Cys
 260 265 270
 Gly Gln Pro Val Tyr Ser Ser Leu Lys Lys Gly Lys Lys Cys Ser Lys
 275 280 285
 Thr Lys Lys Ser Pro Glu Pro Val Arg Phe Thr Tyr Ala Gly Cys Leu
 290 295 300
 Ser Val Lys Lys Tyr Arg Pro Lys Tyr Cys Gly Ser Cys Val Asp Gly
 305 310 315 320
 Arg Cys Cys Thr Pro Gln Leu Thr Arg Thr Val Lys Met Arg Phe Arg
 325 330 335
 Cys Glu Asp Gly Glu Thr Phe Ser Lys Asn Val Met Met Ile Gln Ser
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 <213> Mus musculus

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 <222> (138)..(1181)

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 cctaccgcgt cccgatc atg ctc gcc tcc gtc gca ggt ccc atc agc ctc 170
 Met Leu Ala Ser Val Ala Gly Pro Ile Ser Leu
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 gcc ttg gtg ctc ctc gcc ctc tgc acc cgg cct gct acg ggc cag gac 218
 Ala Leu Val Leu Leu Ala Leu Cys Thr Arg Pro Ala Thr Gly Gln Asp
 15 20 25
 tgc agc gcg caa tgt cag tgc gca gcc gaa gca gcg ccg cac tgc ccc 266
 Cys Ser Ala Gln Cys Gln Cys Ala Ala Glu Ala Ala Pro His Cys Pro
 30 35 40
 gcc ggc gtg agc ctg gtg ctg gac ggc tgc ggc tgc tgc cgc gtc tgc 314
 Ala Gly Val Ser Leu Val Leu Asp Gly Cys Gly Cys Cys Arg Val Cys
 45 50 55
 gcc aag cag ctg gga gaa ctg tgt acg gag cgt gac ccc tgc gac cca 362

Ala 60	Lys	Gln	Leu	Gly	Glu 65	Leu	Cys	Thr	Glu	Arg 70	Asp	Pro	Cys	Asp	Pro 75	
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gga Gly	gtg Val	tgc Cys	act Thr 95	gcc Ala	aaa Lys	gat Asp	ggg Gly	gca Ala 100	ccc Pro	tgt Cys	gtc Val	ttc Phe	ggg Gly 105	ggg Gly	tcg Ser	458
gtg Val	tac Tyr	cgc Arg 110	agc Ser	ggg Gly	gag Glu	tcc Ser	ttc Phe 115	caa Gln	agc Ser	agc Ser	tgc Cys	aaa Lys 120	tac Tyr	caa Gln	tgc Cys	506
act Thr	tgc Cys 125	ctg Leu	gat Asp	ggg Gly	gcc Ala	gtg Val 130	ggc Gly	tgc Cys	gtg Val	ccc Pro	cta Leu 135	tgc Cys	agc Ser	atg Met	gac Asp	554
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gag Glu	tgg Trp 205	agc Ser	gcc Ala	tgt Cys	tct Ser	aag Lys 210	acc Thr	tgt Cys	gga Gly	atg Met	ggc Gly 215	atc Ile	tcc Ser	acc Thr	cga Arg	794
gtt Val 220	acc Thr	aat Asn	gac Asp	aat Asn	acc Thr 225	ttc Phe	tgc Cys	aga Arg	ctg Leu	gag Glu 230	aag Lys	cag Gln	agc Ser	cgc Arg	ctc Leu 235	842
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ggg Gly	gtg Val 285	tgc Cys	aca Thr	gac Asp	ggc Gly	cgc Arg 290	tgc Cys	tgc Cys	aca Thr	ccg Pro	cac His 295	aga Arg	acc Thr	acc Thr	act Thr	1034
ctg Leu 300	cca Pro	gtg Val	gag Glu	ttc Phe	aaa Lys 305	tgc Cys	ccc Pro	gat Asp	ggc Gly	gag Glu 310	atc Ile	atg Met	aaa Lys	aag Lys	aat Asn 315	1082
atg Met	atg Met	ttc Phe	atc Ile	aag Lys	acc Thr	tgt Cys	gcc Ala	tgc Cys	cat His	tac Tyr	aac Asn	tgt Cys	cct Pro	ggg Gly	gac Asp	1130

320

325

330

aat gac atc ttt gag tcc ctg tac tac agg aag atg tac gga gac atg 1178
 Asn Asp Ile Phe Glu Ser Leu Tyr Tyr Arg Lys Met Tyr Gly Asp Met
 335 340 345

gcg taaagccagg aagtaaggga cacgaactca ttagactata acttgaactg 1231
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ctgcttcttt gattatgact gggttggggt ggggggcagt ttatttggtg agagtgtgac 2191

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<212> PRT

<213> Mus musculus

<400> 6

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 35 40 45

Val Leu Asp Gly Cys Gly Cys Cys Arg Val Cys Ala Lys Gln Leu Gly
 50 55 60

Glu Leu Cys Thr Glu Arg Asp Pro Cys Asp Pro His Lys Gly Leu Phe

65	70	75	80
Cys Asp Phe Gly Ser Pro Ala Asn Arg Lys Ile Gly Val Cys Thr Ala	85	90	95
Lys Asp Gly Ala Pro Cys Val Phe Gly Gly Ser Val Tyr Arg Ser Gly	100	105	110
Glu Ser Phe Gln Ser Ser Cys Lys Tyr Gln Cys Thr Cys Leu Asp Gly	115	120	125
Ala Val Gly Cys Val Pro Leu Cys Ser Met Asp Val Arg Leu Pro Ser	130	135	140
Pro Asp Cys Pro Phe Pro Arg Arg Val Lys Leu Pro Gly Lys Cys Cys	145	150	155
Lys Glu Trp Val Cys Asp Glu Pro Lys Asp Arg Thr Ala Val Gly Pro	165	170	175
Ala Leu Ala Ala Tyr Arg Leu Glu Asp Thr Phe Gly Pro Asp Pro Thr	180	185	190
Met Met Arg Ala Asn Cys Leu Val Gln Thr Thr Glu Trp Ser Ala Cys	195	200	205
Ser Lys Thr Cys Gly Met Gly Ile Ser Thr Arg Val Thr Asn Asp Asn	210	215	220
Thr Phe Cys Arg Leu Glu Lys Gln Ser Arg Leu Cys Met Val Arg Pro	225	230	235
Cys Glu Ala Asp Leu Glu Glu Asn Ile Lys Lys Gly Lys Lys Cys Ile	245	250	255
Arg Thr Pro Lys Ile Ala Lys Pro Val Lys Phe Glu Leu Ser Gly Cys	260	265	270
Thr Ser Val Lys Thr Tyr Arg Ala Lys Phe Cys Gly Val Cys Thr Asp	275	280	285
Gly Arg Cys Cys Thr Pro His Arg Thr Thr Thr Leu Pro Val Glu Phe	290	295	300
Lys Cys Pro Asp Gly Glu Ile Met Lys Lys Asn Met Met Phe Ile Lys	305	310	315
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<212> DNA

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<223> CTGF cDNA coding sequence

<220>

<221> CDS

<222> (130)..(1176)

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gtgccaacc	atg	acc	gcc	gcc	agt	atg	ggc	ccc	gtc	cgc	gtc	gcc	ttc	gtg		171
	Met	Thr	Ala	Ala	Ser	Met	Gly	Pro	Val	Arg	Val	Ala	Phe	Val		
	1				5					10						
gtc	ctc	ctc	gcc	ctc	tgc	agc	cgg	ccg	gcc	gtc	ggc	cag	aac	tgc	agc	219
Val	Leu	Leu	Ala	Leu	Cys	Ser	Arg	Pro	Ala	Val	Gly	Gln	Asn	Cys	Ser	
15					20					25					30	
ggg	ccg	tgc	cgg	tgc	ccg	gac	gag	ccg	gcg	ccg	cgc	tgc	ccg	gcg	ggc	267
Gly	Pro	Cys	Arg	Cys	Pro	Asp	Glu	Pro	Ala	Pro	Arg	Cys	Pro	Ala	Gly	
				35					40					45		
gtg	agc	ctc	gtg	ctg	gac	ggc	tgc	ggc	tgc	tgc	cgc	gtc	tgc	gcc	aag	315
Val	Ser	Leu	Val	Leu	Asp	Gly	Cys	Gly	Cys	Cys	Arg	Val	Cys	Ala	Lys	
			50					55					60			
cag	ctg	ggc	gag	ctg	tgc	acc	gag	cgc	gac	ccc	tgc	gac	ccg	cac	aag	363
Gln	Leu	Gly	Glu	Leu	Cys	Thr	Glu	Arg	Asp	Pro	Cys	Asp	Pro	His	Lys	
		65					70					75				
ggc	ctc	ttc	tgt	gac	ttc	ggc	tcc	ccg	gcc	aac	cgc	aag	atc	ggc	gtg	411
Gly	Leu	Phe	Cys	Asp	Phe	Gly	Ser	Pro	Ala	Asn	Arg	Lys	Ile	Gly	Val	
	80					85					90					
tgc	acc	gcc	aaa	gat	ggt	gct	ccc	tgc	atc	ttc	ggt	ggt	acg	gtg	tac	459
Cys	Thr	Ala	Lys	Asp	Gly	Ala	Pro	Cys	Ile	Phe	Gly	Gly	Thr	Val	Tyr	
95					100					105					110	
cgc	agc	gga	gag	tcc	ttc	cag	agc	agc	tgc	aag	tac	cag	tgc	acg	tgc	507
Arg	Ser	Gly	Glu	Ser	Phe	Gln	Ser	Ser	Cys	Lys	Tyr	Gln	Cys	Thr	Cys	
				115					120					125		
ctg	gac	ggg	gcg	gtg	ggc	tgc	atg	ccc	ctg	tgc	agc	atg	gac	gtt	cgt	555
Leu	Asp	Gly	Ala	Val	Gly	Cys	Met	Pro	Leu	Cys	Ser	Met	Asp	Val	Arg	
			130					135					140			
ctg	ccc	agc	cct	gac	tgc	ccc	ttc	ccg	agg	agg	gtc	aag	ctg	ccc	ggg	603
Leu	Pro	Ser	Pro	Asp	Cys	Pro	Phe	Pro	Arg	Arg	Val	Lys	Leu	Pro	Gly	
		145					150					155				
aaa	tgc	tgc	gag	gag	tgg	gtg	tgt	gac	gag	ccc	aag	gac	caa	acc	gtg	651
Lys	Cys	Cys	Glu	Glu	Trp	Val	Cys	Asp	Glu	Pro	Lys	Asp	Gln	Thr	Val	
	160					165					170					
gtt	ggg	cct	gcc	ctc	gcg	gct	tac	cga	ctg	gaa	gac	acg	ttt	ggc	cca	699
Val	Gly	Pro	Ala	Leu	Ala	Ala	Tyr	Arg	Leu	Glu	Asp	Thr	Phe	Gly	Pro	
175					180					185					190	
gac	cca	act	atg	att	aga	gcc	aac	tgc	ctg	gtc	cag	acc	aca	gag	tgg	747
Asp	Pro	Thr	Met	Ile	Arg	Ala	Asn	Cys	Leu	Val	Gln	Thr	Thr	Glu	Trp	
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gtc agg cct tgc gaa gct gac ctg gaa gag aac att aag aag ggc aaa	891
Val Arg Pro Cys Glu Ala Asp Leu Glu Glu Asn Ile Lys Lys Gly Lys	
240 245 250	
aag tgc atc cgt act ccc aaa atc tcc aag cct atc aag ttt gag ctt	939
Lys Cys Ile Arg Thr Pro Lys Ile Ser Lys Pro Ile Lys Phe Glu Leu	
255 260 265 270	
tct ggc tgc acc agc atg aag aca tac cga gct aaa ttc tgt gga gta	987
Ser Gly Cys Thr Ser Met Lys Thr Tyr Arg Ala Lys Phe Cys Gly Val	
275 280 285	
tgt acc gac ggc cga tgc tgc acc ccc cac aga acc acc acc ctg ccg	1035
Cys Thr Asp Gly Arg Cys Cys Thr Pro His Arg Thr Thr Thr Leu Pro	
290 295 300	
gtg gag ttc aag tgc cct gac ggc gag gtc atg aag aag aac atg atg	1083
Val Glu Phe Lys Cys Pro Asp Gly Glu Val Met Lys Lys Asn Met Met	
305 310 315	
ttc atc aag acc tgt gcc tgc cat tac aac tgt ccc gga gac aat gac	1131
Phe Ile Lys Thr Cys Ala Cys His Tyr Asn Cys Pro Gly Asp Asn Asp	
320 325 330	
atc ttt gaa tcg ctg tac tac agg aag atg tac gga gac atg gca	1176
Ile Phe Glu Ser Leu Tyr Tyr Arg Lys Met Tyr Gly Asp Met Ala	
335 340 345	
tgaagccaga gagtgagaga cattaactca ttagactgga acttgaactg attcacatct	1236
cattttttccg taaaaatgat ttcagtagca caagttatctt aaatctgttt ttctaactgg	1296
gggaaaagat tccccaccaa ttcaaaacat tgtgccatgt caaacaata gtctatcttc	1356
cccagacact ggtttgaaga atgttaagac ttgacagtgg aactacatta gtacacagca	1416
ccagaatgta tattaagggtg tggcttttagg agcagtggga gggtagccggc ccggttagta	1476
tcatcagatc gactcttata cgagtaatat gcctgctatt tgaagtgtaa ttgagaagga	1536
aaatttttagc gtgctcactg acctgcctgt agccccagtg acagctagga tgtgcattct	1596
ccagccatca agagactgag tcaagttggt ccttaagtca gaacagcaga ctgagctctg	1656
acattctgat tcgaatgaca ctgttcagga atcggaatcc tgctcgattag actggacagc	1716
ttgtggcaag tgaatttgcc tgtaacaagc cagatTTTTT aaaatttata ttgtaaatat	1776
tgtgtgtgtg tgtgtgtgtg tatatatata tatatatgta cagttatcta agttaattta	1836
aagttgtttg tgccttttta tttttgtttt taatgctttg atatttcaat gttagcctca	1896
atttctgaac accataggta gaatgtaaag cttgtctgat cgttcaaagc atgaaatgga	1956
tacttatatg gaaattctgc tcagatagaa tgacagtccg tcaaaacaga ttgtttgcaa	2016
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<210> 8
 <211> 349
 <212> PRT
 <213> Homo sapiens

<400> 8
 Met Thr Ala Ala Ser₅ Met Gly Pro Val Arg₁₀ Val Ala Phe Val Val₁₅ Leu
 Leu Ala Leu Cys₂₀ Ser Arg Pro Ala Val₂₅ Gly Gln Asn Cys Ser₃₀ Gly Pro
 Cys Arg Cys₃₅ Pro Asp Glu Pro Ala₄₀ Pro Arg Cys Pro Ala₄₅ Gly Val Ser
 Leu Val₅₀ Leu Asp Gly Cys Gly₅₅ Cys Cys Arg Val Cys₆₀ Ala Lys Gln Leu
 Gly₆₅ Glu Leu Cys Thr Glu₇₀ Arg Asp Pro Cys Asp₇₅ Pro His Lys Gly Leu₈₀
 Phe Cys Asp Phe Gly₈₅ Ser Pro Ala Asn Arg₉₀ Lys Ile Gly Val Cys₉₅ Thr
 Ala Lys Asp Gly₁₀₀ Ala Pro Cys Ile Phe₁₀₅ Gly Gly Thr Val Tyr₁₁₀ Arg Ser
 Gly Glu Ser₁₁₅ Phe Gln Ser Ser Cys₁₂₀ Lys Tyr Gln Cys Thr₁₂₅ Cys Leu Asp
 Gly Ala Val₁₃₀ Gly Cys Met Pro₁₃₅ Leu Cys Ser Met Asp₁₄₀ Val Arg Leu Pro
 Ser₁₄₅ Pro Asp Cys Pro Phe₁₅₀ Pro Arg Arg Val Lys₁₅₅ Leu Pro Gly Lys Cys₁₆₀
 Cys Glu Glu Trp Val₁₆₅ Cys Asp Glu Pro Lys₁₇₀ Asp Gln Thr Val Val₁₇₅ Gly
 Pro Ala Leu Ala₁₈₀ Ala Tyr Arg Leu Glu₁₈₅ Asp Thr Phe Gly Pro₁₉₀ Asp Pro
 Thr Met Ile₁₉₅ Arg Ala Asn Cys Leu₂₀₀ Val Gln Thr Thr Glu₂₀₅ Trp Ser Ala
 Cys Ser₂₁₀ Lys Thr Cys Gly Met₂₁₅ Gly Ile Ser Thr Arg₂₂₀ Val Thr Asn Asp
 Asn Ala Ser Cys Arg Leu₂₃₀ Glu Lys Gln Ser Arg₂₃₅ Leu Cys Met Val Arg₂₄₀
 Pro Cys Glu Ala Asp₂₄₅ Leu Glu Glu Asn Ile₂₅₀ Lys Lys Gly Lys Lys₂₅₅ Cys
 Ile Arg Thr Pro₂₆₀ Lys Ile Ser Lys Pro₂₆₅ Ile Lys Phe Glu Leu₂₇₀ Ser Gly
 Cys Thr Ser₂₇₅ Met Lys Thr Tyr Arg₂₈₀ Ala Lys Phe Cys Gly₂₈₅ Val Cys Thr
 Asp Gly₂₉₀ Arg Cys Cys Thr Pro₂₉₅ His Arg Thr Thr Thr₃₀₀ Leu Pro Val Glu
 Phe Lys Cys Pro Asp Gly₃₁₀ Glu Val Met Lys Lys₃₁₅ Asn Met Met Phe Ile₃₂₀
 Lys Thr Cys Ala Cys₃₂₅ His Tyr Asn Cys Pro₃₃₀ Gly Asp Asn Asp Ile₃₃₅ Phe
 Glu Ser Leu Tyr Tyr Arg Lys Met Tyr Gly Asp Met Ala

<210> 9
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<400> 9
 ggggatctgt gacgagccca aggac 25

<210> 10
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<400> 10
 ggaattcga ccaggcagtt ggctcg 26

<210> 11
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<400> 11
 ggggatcctg tgatgaagac agcatt 26

<210> 12
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<400> 12
 ggaattcaa cgatgcattt ctggcc 26

<210> 13
 <211> 21
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: synthetic peptide

<400> 13
 Asp Gly Cys Gly Cys Cys Lys Val Cys Ala Lys Gln Leu Asn Glu Asp
 1 5 10 15

Cys Ser Lys Thr Gln

<210> 14
 <211> 21
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: synthetic peptide

<400> 14
 Pro Asn Cys Lys His Gln Cys Thr Cys Ile Asp Gly Ala Val Gly Cys
 1 5 10 15
 Ile Pro Leu Cys Pro
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<210> 15
 <211> 24
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: synthetic peptide

<400> 15
 Cys Ile Val Gln Thr Thr Ser Trp Ser Gln Cys Ser Lys Ser Cys Gly
 1 5 10 15
 Thr Gly Ile Ser Thr Arg Val Thr
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<210> 16
 <211> 26
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: synthetic peptide

<400> 16
 Ile Ser Thr Arg Val Thr Asn Asp Asn Pro Glu Cys Arg Leu Val Lys
 1 5 10 15
 Glu Thr Arg Ile Cys Glu Val Arg Pro Cys
 20 25

<210> 17
 <211> 21
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: synthetic peptide

<400> 17
 Lys Tyr Cys Gly Ser Cys Val Asp Gly Arg Cys Cys Thr Pro Leu Gln

1	5	10	15
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Thr Arg Thr Val Lys
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<210> 18
 <211> 39
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer fH1

<400> 18
 gcggcatgca gcgcgaccgc gaaatcccca gaaccagtc 39

<210> 19
 <211> 42
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer rH1

<400> 19
 tcgcgctgca tgccgcgccc gcttttaggc tgctgtacac tg 42

<210> 20
 <211> 32
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer fH2

<400> 20
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<210> 21
 <211> 31
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer rH2

<400> 21
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<210> 22
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: upstream PCR
 primer

<400> 22
 cagaccacgt cttggtcc 18

<210> 23
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: downstream PCR primer

<400> 23
gaataggctg tacagtcgg 19

<210> 24
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 24
cacaacagaa gccaggaacc 20

<210> 25
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: lower PCR primer

<400> 25
gaggggacga cgacagtatc 20

<210> 26
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: upper PCR primer

<400> 26
caacggagcc aggggaggtg 20

<210> 27
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: lower wild-type PCR primer

<400> 27
cggcgacaca gaaccaacaa 20

<210> 28
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: lower mutant
PCR primer

<400> 28
gaggggacga cgacagtatc

20

<210> 29
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic
peptide

<400> 29
His His Leu Gly Gly Ala Lys Gln Ala Gly Asp Val
1 5 10

<210> 30
<211> 37
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic
peptide

<400> 30
Ser Leu Lys Ala Gly Ala Ala Cys Ser Ala Thr Ala Lys Ser Pro Glu
1 5 10 15

Pro Val Arg Phe Thr Tyr Ala Gly Cys Ser Ser Val Ala Ala Tyr Ala
20 25 30

Pro Lys Tyr Cys Gly
35

<210> 31
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic
peptide

<400> 31
Gly Arg Gly Asp Ser Pro
1 5

<210> 32
<211> 6
<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic peptide

<400> 32

Gly Arg Gly Glu Ser Pro
1 5

<210> 33

<211> 375

<212> PRT

<213> Chicken

<400> 33

Met Gly Ser Ala Gly Ala Arg Pro Ala Leu Ala Ala Ala Leu Leu Cys
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Leu Ala Arg Leu Ala Leu Gly Ser Pro Cys Pro Ala Val Cys Gln Cys
20 25 30

Pro Ala Ala Ala Pro Gln Cys Ala Pro Gly Val Gly Leu Val Pro Asp
35 40 45

Gly Cys Gly Cys Cys Lys Val Cys Ala Lys Gln Leu Asn Glu Asp Cys
50 55 60

Ser Arg Thr Gln Pro Cys Asp His Thr Lys Gly Leu Glu Cys Asn Phe
65 70 75 80

Gly Ala Ser Pro Ala Ala Thr Asn Gly Ile Cys Arg Ala Gln Ser Glu
85 90 95

Gly Arg Pro Cys Glu Tyr Asn Ser Lys Ile Tyr Gln Asn Gly Glu Ser
100 105 110

Phe Gln Pro Asn Cys Lys His Gln Cys Thr Cys Ile Asp Gly Ala Val
115 120 125

Gly Cys Ile Pro Leu Cys Pro Gln Glu Leu Ser Leu Pro Asn Leu Gly
130 135 140

Cys Pro Ser Pro Arg Leu Val Lys Val Pro Gly Gln Cys Cys Glu Glu
145 150 155 160

Trp Val Cys Asp Glu Ser Lys Asp Ala Leu Glu Glu Leu Glu Gly Phe
165 170 175

Phe Ser Lys Glu Phe Gly Leu Asp Ala Ser Glu Gly Glu Leu Thr Arg
180 185 190

Asn Asn Glu Leu Ile Ala Ile Val Lys Gly Gly Leu Lys Met Leu Pro
195 200 205

Val Phe Gly Ser Glu Pro Gln Ser Arg Ala Phe Glu Asn Pro Lys Cys
210 215 220

Ile Val Gln Thr Thr Ser Trp Ser Gln Cys Ser Lys Thr Cys Gly Thr
225 230 235 240

Gly Ile Ser Thr Arg Val Thr Asn Asp Asn Pro Asp Cys Lys Leu Ile
245 250 255

Lys Glu Thr Arg Ile Cys Glu Val Arg Pro Cys Gly Gln Pro Ser Tyr
260 265 270

Ala Ser Leu Lys Lys Gly Lys Lys Cys Thr Lys Thr Lys Lys Ser Pro
275 280 285

Ser Pro Val Arg Phe Thr Tyr Ala Gly Cys Ser Ser Val Lys Lys Tyr
290 295 300

Arg Pro Lys Tyr Cys Gly Ser Cys Val Asp Gly Arg Cys Cys Thr Pro
305 310 315 320

Gln Gln Thr Arg Thr Val Lys Ile Arg Phe Arg Cys Asp Asp Gly Glu
325 330 335

Thr Phe Thr Lys Ser Val Met Met Ile Gln Ser Cys Arg Cys Asn Tyr
340 345 350

Asn Cys Pro His Ala Asn Glu Ala Tyr Pro Phe Tyr Arg Leu Val Asn
355 360 365

Asp Ile His Lys Phe Arg Asp
370 375

<210> 34
<211> 351
<212> PRT
<213> Avian

<400> 34

Met Glu Thr Gly Gly Gly Gln Gly Leu Pro Val Leu Leu Leu Leu Leu
1 5 10 15

Leu Leu Leu Arg Pro Cys Glu Val Ser Gly Arg Glu Ala Ala Cys Pro
20 25 30

Arg Pro Cys Gly Gly Arg Cys Pro Ala Glu Pro Pro Arg Cys Ala Pro

35

40

45

Gly Val Pro Ala Val Leu Asp Gly Cys Gly Cys Cys Leu Val Cys Ala
50 55 60

Arg Gln Arg Gly Glu Ser Cys Ser Pro Leu Leu Pro Cys Asp Glu Ser
65 70 75 80

Gly Gly Leu Tyr Cys Asp Arg Gly Pro Glu Asp Gly Gly Gly Ala Gly
85 90 95

Ile Cys Met Val Leu Glu Gly Asp Asn Cys Val Phe Asp Gly Met Ile
100 105 110

Tyr Arg Asn Gly Glu Thr Phe Gln Pro Ser Cys Lys Tyr Gln Cys Thr
115 120 125

Cys Arg Asp Gly Gln Ile Gly Cys Leu Pro Arg Cys Asn Leu Gly Leu
130 135 140

Leu Leu Pro Gly Pro Asp Cys Pro Phe Pro Arg Lys Ile Glu Val Pro
145 150 155 160

Gly Glu Cys Cys Glu Lys Trp Val Cys Asp Pro Arg Asp Glu Val Leu
165 170 175

Leu Gly Gly Phe Ala Met Ala Ala Tyr Arg Gln Glu Ala Thr Leu Gly
180 185 190

Ile Asp Val Ser Asp Ser Ser Ala Asn Cys Ile Glu Gln Thr Thr Glu
195 200 205

Trp Ser Ala Cys Ser Lys Ser Cys Gly Met Gly Phe Ser Thr Arg Val
210 215 220

Thr Asn Arg Asn Gln Gln Cys Glu Met Val Lys Gln Thr Arg Leu Cys
225 230 235 240

Met Met Arg Pro Cys Glu Asn Glu Glu Pro Ser Asp Lys Lys Gly Lys
245 250 255

Lys Cys Ile Gln Thr Lys Lys Ser Met Lys Ala Val Arg Phe Glu Tyr
260 265 270

Lys Asn Cys Thr Ser Val Gln Thr Tyr Lys Pro Arg Tyr Cys Gly Leu
275 280 285

Cys Asn Asp Gly Arg Cys Cys Thr Pro His Asn Thr Lys Thr Ile Gln
290 295 300

Val Glu Phe Arg Cys Pro Gln Gly Lys Phe Leu Lys Lys Pro Met Met
305 310 315 320

Leu Ile Asn Thr Cys Val Cys His Gly Asn Cys Pro Gln Ser Asn Asn
325 330 335

Ala Phe Phe Gln Pro Leu Asp Pro Met Ser Ser Glu Ala Lys Ile
340 345 350
